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Research Article

Morphological characterization and assessment of genetic diversity in pigeonpea [Cajanus cajan (L.) Millsp.] germplasm

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Abstract
A total of 243 genotypes of pigeonpea were evaluated during *Kharif,* 2019 on the basis of DUS and D^2-cluster analysis. Pigeonpea genotypes were grown in the augmented design for evaluation. Morphological characterization was done based on plant descriptors for pigeonpea at different stages of plant growth. The cluster analysis grouped all the genotypes into six clusters. The clusters I, II, III, IV, V and VI had 32,3,9,79,115 and 5 genotypes, respectively. The inter cluster distance was maximum between cluster II and VI (240.47) followed by cluster I and II (231.37). On the basis of cluster mean values cluster II was superior for the character pods/plant (340.90) as well as in yield/plant (59.4). The genotypes included in cluster VI were early with short plant height. The study revealed that the diverse genotypes *viz*; AH 06-09, AH 14-01, AH 16-36, PADT-16 and HDM 04-01 could be used in hybridization programme to develop high yielding, early genotypes with short plant height.

Key words: Pigeonpea, DUS, diversity, cluster analysis

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is the second important pulse crop of India after chickpea. Pigeonpea (2n=22) commonly known as arhar, tur, and redgram belongs to the genus *Cajanus*, tribe Phaseoleae, subtribe *Cajaninae*, subfamily Papilionoideae, and family Fabaceae. India is considered as primary centre of origin and diversity for pigeonpea (Vavilov,1926 and Van der Maeson,1990). Pigeonpea ranks sixth in global grain legume production and worldwide it is cultivated in about 6.99 m ha area with an annual production of 5.96 m t and mean productivity of 852 kg/ha (FAOSTAT, 2019). India ranks first in annual pigeonpea production with 4.29 m t followed by Myanmar (0.68 m t), Malawi (0.43 m t) and Kenya (0.085 m t) (FAOSTAT, 2019). It is grown in more than 25 tropical and subtropical countries, either as a sole crop or intercrop with urdbean, mungbean, castor, sorghum, soybean, cotton, maize and groundnut. In India, it is cultivated in states such as Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Uttar Pradesh, Gujarat, Jharkhand, Rajasthan, Punjab and Haryana. Being a legume, the pigeonpea enriches soil through symbiotic nitrogen fixation. Dry grain of the commonly grown cultivars contains 21 to 24% protein and is usually consumed as *dhal*, a type of split peas, and as green peas.

Genetic diversity is the base for the survival of plants in nature and crop improvement. Morphological characterization is useful for the development of the core collection of germplasm (Reddy *et al.,* 2005). Diversity in plant genetic resources provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics (Bhandari *et al.,* 2017). The concept of DUS was fundamental to the characterization of the variety as a unique creation (Sahu *et al*., 2018). D^2 analysis developed by Mahalanobis (1936) was

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used to measure genetic divergence and to classify the germplasm into distinct groups. Therefore, the present investigation was carried out to study genetic and morphological diversity for different characters aimed at isolating desirable genotypes for yield and other characters.

MATERIALS AND METHODS

The present experiment was conducted at the Farm area of the Pulses section of the Department of Genetics and Plant Breeding, CCS HAU Hisar, during *Kharif*, 2019. This is located at a latitude of $29^0 10'$ N and a longitude of $75^0 46'$ E. The experimental material consisted of 236 pigeonpea genotypes, the genotypes were planted in augmented design (ABD 1) in a single row of 4 m length with a spacing of 60 x 20 cm. along with seven check varieties. The data for different morphological traits, yield and yield attributing traits were recorded. The morphological characters were assessed by visual observation of individual plants or plant parts or by single observation of a group of plants in the plot depends upon the character under observation. The data for quantitative traits *viz*., days to 50 per cent flowering, days to maturity, plant height, number of pods per plant, number of branches per plant, 100-seed weight and seed yield per plant was recorded on five random plants in each row. Genetic diversity was estimated as given by Mahalanobis,(1936) and the grouping of germplasm lines into different clusters was done by using the procedure of Rao, (1952).

RESULTS AND DISCUSSION

A total of two hundred and forty three pigeonpea genotypes were characterized based on twenty different morphological characters (**Table 1**). Plant branching pattern was erect in only three genotypes and 240 genotypes were spreading type. The time of flowering was early (61-90 days) in 178 genotypes and medium (91-130 days) in 65 genotypes. All the 243 genotypes were indeterminate in growth habits. The colour of the stem was green for all the genotypes. Leaf shape was observed as oblong in 240 genotypes and 2 genotypes showed obovate type and 1 showed narrowly oblong leaves. Pubescence on a lower surface of the leaf was absent in all genotypes. Flower colour and pattern of streaks on petals (Standard) is also an important character for variety identification. A total of 147 genotypes showed yellow flower colour and 96 genotypes showed light yellow. Van der Maesen (1990) identified six colour classes in pigeonpea flowers. A pattern of streaks on petals (Standard) was absent in 7 genotypes, sparse in 223 genotypes, medium in 12 and dense in one genotype. Out of total of 243 genotypes, only one genotype showed green pod colour, purple pod colour was found in one genotype and other 241 showed green pods with purple streaks. Pod pubescence, waxiness and surface stickiness were absent in all 243 genotypes. Pod constriction was slight in seven genotypes and prominent in the remaining 236 genotypes. Less than 4 cm pod length was observed in 19 genotypes, 4-5 cm pod length was observed in 188 genotypes and the remaining 36 genotypes had more than 5 cm pod length. A number of seeds/pod is an important yield attributing character, 14 genotypes had 3 seeds per pod, 229 genotypes had four seeds/pod. Plant height is an important trait in pigeonpea. Mechanized operations are not feasible and manual harvesting alone consumes about 25-30% of the total labour requirement of the crop. Development of dwarf and extra early variety will allow mechanical harvesting and other operations like spray etc. Out of 243 genotypes, only three were of medium height (100-150 cm) and 240 were tall (>150 cm). Seed characters such as colour-pattern, shape and size are very important for the grouping of genotypes (Copeland and Mc Donald, 2001). Seed colour was found to be cream in one genotype and seed shape was oval for all genotypes. 100 seed weight was less than 7g in 18 genotypes, 7-9 g in 199 genotypes and large (9-11 g) in 26 genotypes.

Analysis of variance for seven quantitative traits was done and findings are presented in **Table 2**. The analysis revealed that the mean sum of squares due to genotypes for all quantitative traits were significantly different. This shows that there was a substantial amount of variability present among the genotypes of pigeonpea for all the traits investigated.The study of genetic divergence among 243 pigeonpea genotypes was performed by employing non-hierachical K-mean cluster analysis method in SPSS software. A total of 243 genotypes were grouped into six different clusters based on seven traits (**Table 3**). Cluster I comprised 32 genotypes, cluster II included 3 genotypes, 9 genotypes were included in cluster III, cluster IV, V and VI were constituted by 79,115 and 5 genotypes, respectively. Thus, cluster V was the largest followed by Cluster IV. The highest inter cluster distance was recorded between cluster II and VI (240.47) followed by Cluster I and II (231.37), cluster IV and II (224.75) and II and V (217.79) (**Table 4**). The cluster mean of seven different morphological characters for six clusters is represented in **Table 5**. All the genotypes in clusters I to V were early maturing (131.6 – 135.8), whereas genotypes falling in cluster VI were extra early in flowering (73.8) and maturity (123.6). The maximum cluster mean value for 100-seed weight was the highest in cluster VI (8.43) followed by cluster V (8.17) and cluster IV (8.15). The maximum cluster means value for plant height was observed in cluster V (249.34), whereas shorter genotypes were found in cluster VI (160.54). The highest cluster mean value was observed for branches/plants in cluster III (8.37) followed by cluster II (8.11). Most number of pods/plant was observed in cluster II (340.90) followed by cluster III (232.63). The maximum cluster means value for yield/plant was in cluster II (59.4) followed by cluster III (39.6). Earlier workers have also reported substantial genetic divergence in pigeonpea germplasm (Rupika and Kannan Bapu, 2014; Satapathy and Panigrahi, 2014; SNCVL *et al.,* 2018; Zavinon *et al.,* 2019; Ranjani *et al.,* 2021)

Table 1. Characterization of 243 pigeonpea genotypes based on morphological characters

S. No.	Morphological Characters	States	Code	Absolute Frequency	Relative Frequency (%)
1.	Plant: Branching Pattern	Erect (<30°)	3	3	1.23
		Semi-spreading (30-60°)	5	240	98.77
		Spreading (>60°)	7	0	0
2.	Time of flowering (50% of the plants with at least one open flower)	Very early (<60 days)	1	0	0
		Early (61-90 days)	3	178	73.25
		Medium (91-130 days)	5	65	26.75
		Late (131- 160 days)	7	0	0
		Very late (>160 days)	9	0	0
3.	Plant: Growth habit	Determinate	1	0	0
		Indeterminate	3	243	100
4.	Stem: Colour	Green	1	243	100
		Purple	2	0	0
5.	Leaf: Shape	Oblong	1	243	100
		Obovate	3	0	0
		Narrowly oblong	5	0	0
6.	Leaf: pubescence on lower surface of the leaf	Absent	1	243	100
		Present	9	0	0
7.	Flower: Colour of base of petal	Light yellow	1	96	39.50
		Yellow	2	147	60.50
		Orange yellow	3	0	0
		Purple	4	0	0
		Red	5	0	0
8.	Flower: pattern of streaks on petal (standard)	Absent	1	7	2.88
		Sparse	3	223	91.77
		Medium	5	12	4.94
		Dense	7	1	0.41
		Mosaic	9	0	0
9.	Pod: Colour	Green	1	1	0.41
		Green with brown streaks	2	0	0
		Green with purple streaks	3	242	99.59
		Purple	4	0	0
		Dark purple	5	0	0
10.	Pod: Pubescence	Absent	1	0	0
		Present	9	243	100
11.	Pod: Waxiness	Absent	1	243	100
		Present	9	0	0
12.	Pod: Surface stickiness	Absent	1	243	100
		Present	9	0	0
13.	Pod: Constriction	Slight	3	0	0
		Prominent	7	243	100
14.	Pod: Size (cm)	< 4 cm	3	19	7.82
		4-5 cm	5	188	77.37
		>5 cm	7	36	14.81
15.	Pod: No. of seeds	2	3	0	0
		3	5	14	5.76
		4	7	229	94.24
16.	Plant: Height	Short(<100 cm)	3	0	0
		Medium (100-150 cm)	5	3	1.23
		Tall (>150 cm)	7	240	98.77
17.	Seed: Colour	Cream	1	1	0.41
		Brown	2	240	98.77
		Dark brown	3	2	0.82
		Grey	4	0	0
		Purple	5	0	0
18.	Seed: Colour pattern	Uniform	1	243	100
		Mottled	2	0	0
19.	Seed: Shape	Oval	1	243	100
		Globular	2	0	0
		Elongate	3	0	0
20.	Seed: Size (100 seed weight)	Small(<7g)	3	18	7.41
		Medium(7-9g)	5	199	81.89
		Large(9-11g)	7	26	10.70
		Very large (>11g)	9	0	0

Table 2. Analysis of variance for various morphological traits of pigeonpea genotypes

		Mean sum of square						
Source of variation	**DF**	**Days to 50 % flowering**	**Days to maturity**	**100 seed weight**	**Plant height**	**Branches/plant**	**Pods/plant**	**Yield/plant**
Block	8	0.19	0.23	0.01	3.77	0.25	15.23	0.36
Genotypes	242	50.39**	47.40**	0.64**	399.30**	3.06**	1536.27**	100.39**
Error	48	0.17	0.20	0.01	3.06	0.21	14.07	0.32
				Contrast analysis				
Among Control	6	319.81**	143.85**	6.70**	6539.14**	8.62**	19830.32**	664.02**
Among Genotypes	235	45.09**	35.59**	0.55**	297.82**	2.92**	1036.26**	76.35**
Control vs Genotype	1	352.47**	3050.55**	0.22**	277.63**	74.72**	19547.14**	2738.88**

**Significant (p=0.01)

Table 3. Grouping of Pigeonpea genotypes in various clusters on the basis of D^2 values

S. No	Clusters	Genotypes	Name of Genotypes
1.	I	32	H 88-12, H 88-41, H 90-04, H 90-13, H 91-12-01, H 91-23, H 93-22, H 93-39, H 93-43, H 99-1, H 99-2, H 99-4, H 00-34, H 00-37, H 01-3, H 01-4, H 01-12, H 01-24, H 02-20, H 02-52, H 04-26, AL 345-22, AL 601, AL 609, AL 1577, AL 1590, ASJ 1009, A 293-4, PUSA 2018-4, IPA 15-06, IPA 15-01, AH 17-17
2.	II	3	H 05-11, AH 06-09, AH 14-01
3.	III	9	AL 13, AL 265, AL 283, AL 1404, AL 2028, ICPL 8500, ICPL 28323, D-5, Paras
4.	IV	79	H 91-10, H 93-08, H 93-13, H 93-24, H 00-8, H 00-15, H 00-28, H 00-40, AL 1992, H 01-8, H 01-9, H 01-11, H 01-14, H 01-33, H 01-36, H 01-37, H 01-122, H 02-39, H 02-43, H 02-63, H 03-29, H 04-21, H 04-24, PA 477, H 05-06, H 05-10, H 05-15, H 05-36, 05-63, H 09-47, AH 02-60, AH 06-02, AH 06-04, AH 06-05, PUSA 2018, AH 06-10, PUSA 2018-3, AH 09-13, PUSA 2018-2, AH 10-08, AH 10-17, AH 10-39, AL 345, AL 668, AL 1259-2-3, AL 1322-6-5-2, AL 1401, AL 1425, AL 1431, AL 1444, AL 1452, AL 1600, AL 1685, KAE 17, ICPL 85012, ICPL 89011-1, ICPL 91008, ICPL 90036, PUSA 84-P3, PUSA 855-2, PUSA 945, PUSA 2002, PUSA 2015-1, PUSA 7601, D-3, CRG 14-07, ASJ 502, PAU 3-1, IPAM 16-1, P 33-3, Bhagvla, EKD 12, PA 536, RKPV 704, IPA 15-03, AH 17-28, AH 17-01, AH 16-02, AH 17-27
5.	V	115	H 00-38, H 02-60, H 02-62, H 02-65, H 03-41, H 04-20, H 05-37, H 05-39, H 05-70, H 07-04, H 08-148, AH 01-04, PUSA 2017, AH 05-12, RKPV 413-02, AH 05-38A, AH 05-46, AL 2207, AH 05-67, AH 06-01, AH 06-03, PA 619, AH 06-07, AH 07-06, AH 07-07, AH 09-01, AH 09-04, AH 09-06, AH 09-08, AH 09-10, AH 09-31, AH 09-33, AH 09-35, AH 09-36, AH 09-38, AH 09-44, AH 09-45, AH 09-46, AH 10-13, AH 10-27, AH 10-29, AH 10-30, AL 311-6, AL 344-1, AL 360-5, AL 442, AL 1095-2-2, AL 1313, AL 1313-2-2, AL 1323-1-2, AL 1336-7-7, AL 1354-2-2, AL 1356-04, AL 1359-03, AL 1362-1, AL 1366-1, AL 1389, AL 1416, AL 1417, AL 1419, AL 1421, AL 1434, AL 1439, AL 1455, AL 1484, AL 1502, AL 1508, AL 1581, AL 1589, AL 1604, AL 1614, AL 1922, ICPL 87, ICPL 9102, ICPL 87008, ICPL 88039, ICPL 91007, ICPL 91053-1, ICPL 92034, ICPL 91039, ICPL 92040, PUSA 204-1, PUSA 204-2, PUSA 2008-2, PUSA 2015-2, PUSA 2016-2, PA 414, PA 421, PA 443, ASJ 123, A 12-01, Harsana, CORG 9701, SC 190306, Scl-285, Sl 83006, Vmb N-1, B 17200 Imp, Exn-13, SJP 102, CRG 2012-20, VRG 13-001, Manak, PAU 881, PUSA 992, UPAS 120, VLA 1, IPA 16E10, AL 2211, RKPV 705, IPA 17E-1, PUSA 2018-5, BP 16-261, PA 554, IPA 15-07
6.	VI	5	ICPL 20338, PADT-16, AH 16-36, AH 16-21, HDM 04-01

Table 4. Average inter-cluster distances for Pigeonpea genotypes

Cluster	I	II	III	IV	V	VI
I		231.377	123.973	20.222	35.585	58.508
II	231.377		110.262	224.753	217.798	240.471
III	123.973	110.262		115.294	107.663	145.599
IV	20.222	224.753	115.294		15.730	76.587
V	35.585	217.798	107.663	15.730		90.863
VI	58.508	240.471	145.599	76.587	90.863	

Table 5. Cluster mean of different characters in Pigeonpea genotypes

	Clusters					
	I	II	III	IV	V	VI
Days to 50 % flowering	87.8	82.0	86.4	86.3	87.7	73.8
Days to maturity	135.8	133.7	131.6	134.7	134.7	123.6
100 seed weight (g)	7.77	7.75	7.18	8.15	8.17	8.43
Plant height(cm)	215.81	244.56	248.71	235.28	249.34	160.54
Branches/plant	6.18	8.11	8.37	6.24	6.84	6.40
Pods/plant	115.08	340.90	232.63	119.80	126.67	119.30
Yield/plant (g)	18.5	59.4	39.6	20.4	20.9	20.8

The above results concluded that maximum genetic divergence was observed between cluster II and VI followed by cluster I and II and cluster IV and II. On the basis of cluster mean values, cluster II was superior for pods/plant and yield/plant, and cluster VI contains early and short plant height genotypes. Cluster VI was superior in 100-seed weight followed by clusters V and IV. This variability can be used for the production of high yielding, early and short pigeonpea varieties. The study revealed that the diverse genotypes *viz*; AH 06-09, AH 14-01, Manak, AH 16-36, PADT-16 and HDM 04-01 can be used in hybridization programme to develop high yielding, early genotypes with short plant height which can easily fit in the crop rotation of NWPZ and feasible for mechanical harvesting.

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